
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=2; day=19; hr=9; min=42; sec=47; ms=323;]

Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and the proteins SEQID (11)

E321 No. of Bases conflict, this line has no nucleotides

SEQID (11) POS (126)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides

SEQID (12) POS (0)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (12)

E321 No. of Bases conflict, this line has no nucleotides SEQID (12) POS (512)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (22)

E321 No. of Bases conflict, this line has no nucleotides SEQID (22) POS (112)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (24)

E321 No. of Bases conflict, this line has no nucleotides SEQID (24) POS (496)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (28)

E321 No. of Bases conflict, this line has no nucleotides SEQID (28) POS (16)

E355 Empty lines found between the amino acid numbering and the proteins SEQID (30)

E321 No. of Bases conflict, this line has no nucleotides SEQID (30) POS (48)

```
<210> 11
<211> 1582
<212> DNA
<213> Zea mays
<220>
<221> CDS
<222> (10)..(1563)
<223> Shrunken-2 gene revertant form
<220>
<221> variation
<222> (267)
\langle 223 \rangle k = g or t; amino acid 86 = Ala.
<220>
<221> variation
<222> (1368)
\langle 223 \rangle r = a or g; amino acid 453 = Pro.
<220>
<221> variation
<222> (1578)
\langle 223 \rangle k = q or t.
* * * * * * * * *
gtt gga gga tgt tac agg ctt att gat atc cct atg agt aac tgc ttc
                                                                       387
Val Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met Ser Asn Cys Phe
                 115
                                                            125
                                      120
aac agt ggt ata aat aag ata ttt gtg atg agt cag ttc aat tct act
                                                                       435
Asn Ser Gly Ile Asn Lys Ile Phe Val Met Ser Gln Phe Asn Ser Thr
                                                        140
             130
                                  135
tog ctt aac cgc cat att cat cgt aca tac ctt gaa ggc ggg atc aac
                                                                       483
Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Glu Gly Gly Ile Asn
                              150
        145
                                                   155
For SEQ ID # 11, 12, 22, 24, 28, and 30 the sequence rules specify the
numbering for amino acids be placed below the line of amino acids in a
protein or coding region of a nucleotide sequence.
```

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino

(a) The symbols and format to be used for nucleotide and/or amino

acid sequence data.

acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

- (d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.
- (4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, prosequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID numbers listed above there are blank lines found between the amino acids and the numbering for the amino acids at different locations. Please remove all blank lines found between the amino acids and the numbering in these sequences.

2.								
E300	Invalid	codon	found	Asn	SEQID	(11)	POS:	388
E300	Invalid	codon	found	Ser	SEQID	(11)	POS:	391
E300	Invalid	codon	found	Gly	SEQID	(11)	POS:	394
E300	Invalid	codon	found	Ile	SEQID	(11)	POS:	397
E300	Invalid	codon	found	Asn	SEQID	(11)	POS:	400
E300	Invalid	codon	found	Lys	SEQID	(11)	POS:	403
E300	Invalid	codon	found	Ile	SEQID	(11)	POS:	406
E300	Invalid	codon	found	Phe	SEQID	(11)	POS:	409
E300	Invalid	codon	found	Val	SEQID	(11)	POS:	412
E300	Invalid	codon	found	Met	SEQID	(11)	POS:	415
E300	Invalid	codon	found	Ser	SEQID	(11)	POS:	418
E300	Invalid	codon	found	Gln	SEQID	(11)	POS:	421
E300	Invalid	codon	found	Phe	SEQID	(11)	POS:	424
E300	Invalid	codon	found	Asn	SEQID	(11)	POS:	427
E300	Invalid	codon	found	Ser	SEQID	(11)	POS:	430
E300	Invalid	codon	found	Thr	SEQID	(11)	POS:	433

The errors shown above are ok and require no response.

********	*******	*****	

Validated By CRFValidator v 1.0.3

Application No: 10569000 Version No: 1.0

Input Set:

Output Set:

Started: 2010-02-18 13:09:42.494 **Finished:** 2010-02-18 13:09:51.451

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms

Total Warnings: 0
Total Errors: 302

No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Err	or code	Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (11)
E	300	Invalid codon found Asn SEQID (11) POS: 388
E	300	Invalid codon found Ser SEQID (11) POS: 391
E	300	Invalid codon found Gly SEQID (11) POS: 394
E	300	Invalid codon found Ile SEQID (11) POS: 397
E	300	Invalid codon found Asn SEQID (11) POS: 400
E	300	Invalid codon found Lys SEQID (11) POS: 403
E	300	Invalid codon found Ile SEQID (11) POS: 406
E	300	Invalid codon found Phe SEQID (11) POS: 409
E	300	Invalid codon found Val SEQID (11) POS: 412
E	300	Invalid codon found Met SEQID (11) POS: 415
E	300	Invalid codon found Ser SEQID (11) POS: 418
E	300	Invalid codon found Gln SEQID (11) POS: 421
E	300	Invalid codon found Phe SEQID (11) POS: 424
E	300	Invalid codon found Asn SEQID (11) POS: 427
E	300	Invalid codon found Ser SEQID (11) POS: 430
E	300	Invalid codon found Thr SEQID (11) POS: 433
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (12)

Input Set:

Output Set:

Started: 2010-02-18 13:09:42.494 **Finished:** 2010-02-18 13:09:51.451

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms

Total Warnings: 0

Total Errors: 302

No. of SeqIDs Defined: 42

Actual SeqID Count: 42

Err	or code	Error Description
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (12)
E	336	Empty lines found between the proteins and the dna
Ε	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna
E	336	Empty lines found between the proteins and the dna This error has occured more than 20 times, will not be displayed

Input Set:

Output Set:

Started: 2010-02-18 13:09:42.494 **Finished:** 2010-02-18 13:09:51.451

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 957 ms

Total Warnings: 0
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Err	or code	Error Description
E	355	Empty lines found between the amino acid numbering and the
Ε	321	No. of Bases conflict, this line has no nucleotides SEQID (22)
Ε	355	Empty lines found between the amino acid numbering and the
Ε	321	No. of Bases conflict, this line has no nucleotides SEQID (24)
Ε	355	Empty lines found between the amino acid numbering and the
Ε	321	No. of Bases conflict, this line has no nucleotides SEQID (28)
Ε	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (30)

```
<110> University of Florida Research Foundation, Inc.
      Hannah, L. Curtis
      Lyerly Linebarger, Carla R.
<120> Heat Stable Variants of Adenosine Diphosphate Glucose Pyrophosphorylase
<130> UF-371XC1 PCT
<140> 10569000
<141> 2010-02-18
<150> US 60/496,188
<151> 2003-08-18
<160> 42
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<213> zea mays
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                                                                     120
gctcatgata gtgttcttgg aatcattctg ggaggtggtg ctgggactag attgtacccc
                                                                     180
ttgacaaaga agcgtgccaa gcctgcagtg ccattgggtg ccaactatag actgattgat
                                                                     240
attectytea geaattytet caacagcaac atatecaaga tetatytyet aacgcaattt
                                                                     300
aactctgctt ccctcaaccg tcacctctca agagcctacg ggagcaacat tggagggtac
                                                                     360
aagaatgaag ggtttgttga agtcttagct gcacagcaga gcccagataa tccaaactgg
                                                                     420
tttcagggta ctgcagatgc tgtaaggcag tacttgtggt tgtttgagga gcataatgtg
                                                                     480
atggaatttc taattcttgc tggcgatcac ctgtaccgga tggactatga aaagttcatt
                                                                     540
caggcacaca gagaaacaaa tgctgatatt accgttgctg ccctaccgat ggatgagaaa
                                                                     600
cgtgcaactg catttggcct catgaaaatt gatgaagaag ggaggatcat tgagtttgct
                                                                     660
gagaaaccga aaggagagca gttgaaagca atgatggttg acaccaccat acttggcctt
                                                                     720
gatgacgtga gggcaaagga aatgccttat attgctagca tgggtatcta tgttttcagc
                                                                     780
aaagatgtaa tgcttcagct cctccgtgaa caatttcctg aagccaatga ctttggaagt
                                                                     840
gaggttattc caggtgcaac cagcattgga aagagggttc aggcttatct gtatgatggt
                                                                     900
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tactgggaag atatcggtac cattgcggca ttttataatg caaacttggg aataaccaag

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cacctgccac cttcaaaggt tcttgatgct gatgtgacag acagtgttat tggtgaagga	1080
tgtgttatta aaaactgcaa gataaaccat tctgtagttg gactccgatc ttgcatatct	1140
gaaggtgcta tcatagagga cagtttacta atgggtgcgg actactatga gacagaagct	1200
gataaaaaac teettgeega aaaaggtgge atteetattg gtattgggaa aaatteatge	1260
atcaggagag caatcattga caagaatgct cgaattggag acaatgttaa gatactcaat	1320
gctgacaatg ttcaagaagc tgcaatggag acagacgggt acttcatcaa aggtggaatt	1380
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Color Lea Mayo	
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Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn	
20 25 30	
Asp Ser Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly Ile 35 40 45	
33 40 43	
Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys	
50 55 60	
Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp	
65 70 75 80	

Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val

Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala

Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val

Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr

Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val

Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr

155

170

85

115

145

100 105

120

130 135 140

150

165

Glu Lys Phe	Ile Gln 180	Ala His	_	Glu Th 185	r Asn	Ala	Asp	Ile 190	Thr	Val
Ala Ala Leu 195	Pro Met	Asp Glu	Lys 2	Arg Al	a Thr	Ala	Phe 205	Gly	Leu	Met
Lys Ile Asp 210	Glu Glu	Gly Arg 215	Ile :	Ile Gl	u Phe	Ala 220	Glu	Lys	Pro	ГÀЗ
Gly Glu Gln 225	Leu Lys	Ala Met 230	Met ¹	Val As	p Thr 235	Thr	Ile	Leu	Gly	Leu 240
Asp Asp Val	Arg Ala 245	Lys Glu	Met I	Pro Ty 25		Ala	Ser	Met	Gly 255	Ile
Tyr Val Phe	Ser Lys 260	Asp Val		Leu Gl 265	n Leu	Leu	Arg	Glu 270	Gln	Phe
Pro Glu Ala 275	Asn Asp	Phe Gly	Ser (Glu Va	l Ile	Pro	Gly 285	Ala	Thr	Ser
Ile Gly Lys 290	Arg Val	Gln Ala 295	Tyr I	Leu Ty	r Asp	300	Tyr	Trp	Glu	Asp
Ile Gly Thr 305	Ile Ala	Ala Phe 310	Tyr 2	Asn Al	a Asn 315	Leu	Gly	Ile	Thr	193 320
Lys Pro Ile	Pro Asp 325	Phe Ser	Phe 5	Tyr As 33		Phe	Ala	Pro	Ile 335	Tyr
Thr Gln Pro	Arg His	Leu Pro		Ser Ly 345	s Val	Leu	Asp	Ala 350	Asp	Val
Thr Asp Ser 355	Val Ile	Gly Glu	Gly (Cys Va	l Ile	Lys	Asn 365	Cys	Lys	Ile
Asn His Ser 370	Val Val	Gly Leu 375	Arg:	Ser Cy	s Ile	Ser 380	Glu	Gly	Ala	Ile
Ile Glu Asp 385	Ser Leu	Leu Met 390	Gly A	Ala As	р Туг 395	Tyr	Glu	Thr	Glu	Ala 400
Asp Lys Lys	Leu Leu 405	Ala Glu	Lys (Gly Gl 41	_	Pro	Ile	Gly	Ile 415	Gly
Lys Asn Ser	Cys Ile 420	Arg Arg		Ile Il 425	e Asp	TÀR	Asn	Ala 430	Arg	Ile
Gly Asp Asn 435	Val Lys	Ile Leu	Asn 440	Ala As	p Asn	Val	Gln 445	Glu	Ala	Ala
Met Glu Thr 450	Asp Gly	Tyr Phe 455	Ile I	Lys Gl	y Gly	11e 460	Val	Thr	Val	Ile
Lys Asp Ala 465	Leu Leu	Pro Ser 470	Gly :	Thr Va	1 Ile 475					

<210> 3

<211> 1425

<212> DNA

<213> zea mays

<400> 3

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gtcacagtga tcaaggatgc tttactccct agtggaacag ttata

60

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<21		475													
<212	2> 1	PRT													
<213	3> :	zea r	mavs												
	-														
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1				5			-3 -		10				1-	15	
Thr	Ala	Ala	Glu	Gln	Pro	Tle	Pro	Lvs	Ara	Asp	Lvs	Ala	Ala	Ala	Asn
			20					25	5	1-			30		
Asp	Ser	Thr	Cvs	Leu	Asn	Pro	Gln	Ala	His	Asp	Ser	Val	Leu	Glv	Tle
Пор	201	35	010	Lea	11011		40	1110		11010	001	45	200	013	
		,,,					10					13			
Tle	T.e11	Gly	Glv	Glv	Δla	Glv	Thr	Ara	T.e.11	Tur	Pro	T.e11	Thr	Lvs	T.vs
110	50	OLy	013	Oly	1110	55	1111	1119	Lea	- <u>y</u> -	60	шец		шур	<u> </u>
	30					33					00				
Ara	Δla	Lys	Pro	Δla	Val	Pro	T.011	Glv	Δla	Δan	Tur	Δrα	T.011	Tlo	Zen
65	1114	шур	110	11±G	70	110	шси	OLy	231G	75	ı yı	1119	шси	110	80
0.5					, 0					, 5					00
Tlo	Pro	Val	Ser	Δan	Cve	T.011	Zan	Sar	Δen	Tlo	Sar	T.v.e	Tla	Tur	Val
116	FIO	vai	SET	85	СУЗ	цец	ASII	Set	90	116	Set	пуз	116	95	vai
				0.5					90					93	
Tou	Thr	Cln	Dho	7 00	Cor	71-	Cor	Lou	7 an	7 2501	шіа	T 011	Cor	λνα	71-
ьец	TIII	Gln	100	ASII	ser	нта	ser	105	ASII	AIG	птъ	ьеи		AIG	Ala
			100					100					110		
Tur	C1,,	Can	7 an	Tlo	C1	C1,,	Т.т.	Tuc	7 an	C1	C1.,	Dha	77.3	C1,,	77.2.7
тут	GIY	Ser	Mali	116	GLY	GIĀ		пур	Maii	GIU	GIY		vai	GIU	vai
		115					120					125			
T 0.11	71.	71-	C1.	C1 =	C - 22	Dao	7 ~ ~	7 ~~~	Dag	7 ~~	Т 2020	Dha	Clm	C1	The
ьец		Ala	GIII	GIII	ser		Asp	ASII	PIO	ASII	_	Pile	GIII	GIĀ	1111
	130					135					140				
3.1 -	3	71-	77-7	3	G1	m	T		T	DI.	G1	G 1	TT -	3	TT - 7
	Asp	Ala	vai	Arg		ıyr	Leu	rrp	Leu		GIU	G±u	HIS	Asn	
145					150					155					160
	~ 3	_,	_	- 1	_		~ 1	_		_	_	_			_
Met	Glu	Phe	Leu		Leu	Ala	GLy	Asp		Leu	Tyr	Arg	Met		Tyr
				165					170					175	
	_	_,					_		_,	_		_	- 1		
GLu	Lys	Phe		Gln	Ala	Hls	Arg		Thr	Asn	Ala	Asp		Thr	Val
			180					185					190		
		_	_		_		_	_						_	
Ala	Ala	Leu	Pro	Met	Asp	Glu	_	Arg	Ala	Thr	Ala		GLy	Leu	Met
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Lys		Asp	Glu	Glu	Gly	_	Ile	Ile	Glu	Phe		Glu	Lys	Pro	Lys
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225					230					235					240

Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile 245 250 250 255

Tyr	Val	Phe	Ser 260	Lys	Asp	Val	Met	Leu 265	Gln	Leu	Leu	Arg	Glu 270	Gln	Phe	
Pro	Glu	Ala 275	Asn	Asp	Phe	Gly	Ser 280	Glu	Val	Ile	Pro	Gly 285	Ala	Thr	Ser	
	Gly 290	Lys	Arg	Val	Gln	Ala 295	Tyr	Leu	Tyr	Asp	Gly 300	Tyr	Trp	Glu	Asp	
Ile 305	Gly	Thr	Ile	Ala	Ala 310	Phe	Tyr	Asn	Ala	Asn 315	Leu	Gly	Ile	Thr	Lys 320	
Lys	Pro	Ile	Pro	Asp 325	Phe	Ser	Phe	Tyr	Asp 330	Arg	Phe	Ala	Pro	Ile 335	Tyr	
Thr	Gln	Pro	Arg 340	His	Leu	Pro	Pro	Ser 345	Lys	Val	Leu	Asp	Ala 350	Asp	Val	
Thr	Asp	Ser 355	Val	Ile	Gly	Glu	Gly 360	Суз	Val	Ile	Lys	Asn 365	Суз	Lys	Ile	
	His 370	Ser	Val	Val	Gly	Leu 375	Arg	Ser	Суз	Ile	Ser 380	Glu	Gly	Ala	Ile	
Ile 385	Glu	Asp	Ser	Leu	Leu 390	Met	Gly	Ala	Asp	Tyr 395	Tyr	Glu	Thr	Glu	Ala 400	
Asp	Lys	Lys	Leu	Leu 405	Ala	Glu	Lys	Gly	Gly 410	Ile	Pro	Ile	Gly	Ile 415	Gly	
Lys	Asn	Ser	Cys 420	Ile	Arg	Arg	Ala	Ile 425	Ile	Asp	Lys	Asn	Ala 430	Arg	Ile	
Gly	Asp	Asn 435	Val	Lys	Ile	Leu	Asn 440	Ala	Asp	Asn	Val	Gln 445	Glu	Ala	Ala	
	Glu 450	Thr	Asp	Gly	Tyr	Phe 455	Ile	Lys	Gly	Gly	Ile 460	Val	Thr	Val	Ile	
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Met Asp Met Ala Leu Ala Ser Lys Ala Ser Pro Pro Pro Trp Asn Ala

Thr Ala Ala Glu Gln Pro Ile Pro Lys Arg Asp Lys Ala Ala Ala Asn \$20\$ \$25\$ \$30\$

Asp Ser Gln Thr Tyr Leu Asn Pro Gln Ala His Asp Ser Val Leu Gly

Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn Val Met Glu Phe Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asn Ala Asp Ile Thr Val Ala Ala Leu Pro Met Asp Glu Lys Arg Ala Thr Ala Phe Gly Leu Met Lys Ile Asp Glu Glu Gly Arg Ile Ile Glu Phe Ala Glu Lys Pro Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly Ile Tyr Val Phe Ser Lys Asp Val Met Leu Gln Leu Leu Arg Glu Gln Phe Pro Glu Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr 275 280 285 Ser Ile Gly Lys Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu Asp Ile Gly Thr Ile Ala Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Phe Ala Pro Ile

Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp

340 345 350

Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys 355 360 365

- Ile Asn His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala 370 375 380
- Ile Ile Glu Asp Ser Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu 385 390 395 400
- Ala Asp Lys Lys Leu Leu Ala Glu Lys Gly Gly Ile Pro Ile Gly Ile 405 410 415
- Gly Lys Asn Ser Cys Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg \$420\$